1. **Purpose**: This document provides the procedure to calculate statistical data on mixed DNA samples that cannot be sorted by component analysis.

2. **Scope:** Qualified DNA Analysts in the NCSBI Forensic Biology Section may use this procedure to perform statistical analysis on DNA mixtures.

3. **Safety:** No safety implications.

4. **Definitions:**

   Combined Probability of Exclusion: The probability that a given DNA type would be excluded as a contributor to a mixed sample.

   Combined Probability of Inclusion: The probability that a given DNA type would be included as a contributor to a mixed sample.

5. **Reference Documents**

   "Approaches to Statistical Analysis of Mixtures and Degraded DNA". pp. 519 - 528. Butler, J. 2005. "Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers". Second Ed. Elsevier Academic Press.

   "Document Control Procedure", NCSBI Forensic Biology Unit SOP.

   "Forensic Inference from Genetic Markers".   Devlin, B. (1992) *Statistical Methods in Medical Research*, 2, 241-262.

   "Interpretation of Complex Forensic DNA Mixtures". Ladd, C., Lee, H.C., Yang, N. and Bieber, F.R. (2001) *Croatian Medical Journal*, 42 (3), 244-246

   "Procedure for completion of Quality System Documents", NCSBI Forensic Biology Unit SOP.

   "Statistical and population genetic issues affecting the evaluation of the frequency of occurrence of DNA profiles calculated from pertinent population databases(s)." DNA Advisory Board (2000), *Forensic Science Communications*, July 2000.

6. Procedure:

6.1. <u>Formulas for CPE</u>: If an evidence sample includes three alleles at a locus (A_1, A_2, A_3) then:

6.1.1. $P = A_1 + A_2 + A_3$ and

6.1.2. $Q = 1 - p$

6.1.3. $PE = [Q^2 + Q(1-Q)\ \theta] + [2Q(1-Q)(1-\theta)]$ $\theta=0.01$

6.1.4. The probability of exclusion (PE) is calculated at each locus and then the PEs from the multiple loci are combined through the following equation:

$$CPE = 1 - [(1 - PE_1) \times (1 - PE_2) \times \ldots (1 - PE_n)]$$

6.2. <u>Calculating CPE using NCSBI CPE Excel Program</u>:

6.2.1. Using the NCSBI CPE Program, choose the "Mixtures-CPE" tab.

6.2.2. Click on the "Clear" tab at the top left section of the spreadsheet to ensure all previous entries are clear.

6.2.3. Enter SBI Case number and Item number in "Case Information" box.

6.2.4. QC Check

6.2.4.1. Enter Expected Results for 9947A/MJB. Note: Population frequency data for D2S1338 and D19S433 have not been determined for the NC Populations and will not be used for calculations.

6.2.4.2. Determine if CPI values are correct. If values are correct, then the program may be used for CPE Calculations.

6.2.4.3. Expected values for 9947A/MJB Mixture:

Race	CPI Results
NC Caucasian	1 in 50.17 Million
NC Black	1 in 9.66 Billion
NC Hispanic	1 in189.33 Million
NC Lumbee Indian	1 in 70.16 Million

6.2.5. Click on the "Clear" tab at the top left section of the spreadsheet to ensure all previous entries are clear.

6.2.6. Enter the allele calls for each locus used in the CPE Calculations. Note: Population frequency data for D2S1338 and D19S433 have not been determined for the NC Populations and will not be used for calculations.

6.2.7. Print the sheets at a part of the permanent case records.

Appendices: 9947A/MJB Mixture for QC Check.

Document Revision History		
Revision Number	**Date**	**Reason**
00	1/30/07	New Document

APPROVAL SIGNATURES	Date
Author/Title (Print)	
(Signature)	
Name/Title (Print)	
(Signature)	
Name/Title (Print)	
(Signature)	

9947A/MJB Mixture for QC Check of NCSBI CPE Statistics Program			
Markers	**9947A/MJB Mixture**		
D8S1179	11	13		
D21S11	29	30		
D7S820	8	10	11	
CSF1PO	10	12		
D3S1358	14	15	17	
THO1	8	9.3		
D13S317	8	9	11	
D16S539	11	12		
D2S1338	--	--	--	--
D19S433	--	--	--	--
vWA	17	18		
TPOX	8	11		
D18S51	13	15	16	19
D5S818	11			
FGA	20	23	24	